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OM of: US-08-962-560A-4 to: N_Geneseq_36:*   out_format : pfs

Date: Feb 5, 2000  8:38 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -Q=/cgn1_1/USPTO_spool/US08962560/runat_03022000_141841_3613/app_query.fasta.1
 -DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=rng -GAPOP=12.000
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
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 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
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 -MAXLEN=1000000 -USER=US08962560 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-08-962-560A-4
Query length: 212
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 1063.640000


score_list:
Sequence            Strd Orig    ZScore    EScore Len  ! Documentation  ..
N_Geneseq_36:V38659  + 1107.00 1425.53  8.4e-72   1235  ! Mus musculus SOCS1 gene. Suppr
N_Geneseq_36:V42701  + 1093.00 1408.54  7.4e-71   1087  ! cDNA encoding a STAT function
N_Geneseq_36:V38663  + 1073.00 1374.61  5.8e-69   2807  ! Rattus norvegicus SOCS1 gene.
N_Geneseq_36:V38662  + 1053.50 1357.47  5.2e-68   1094  ! Homo sapiens SOCS1 gene. Suppr
N_Geneseq_36:T43380  +  249.50  314.06  6.8e-10   1960  ! Human cytokine response gene C
N_Geneseq_36:V38660  +  234.50  299.46  4.4e-09   1121  ! Mus musculus SOCS2 gene. Suppr
N_Geneseq_36:V69307  +  234.50  293.17  9.9e-09   2342  ! Human EPRG1 cDNA #1. New EPO p
N_Geneseq_36:V69309  +  234.50  293.17  9.9e-09   2342  ! Human EPRG1 cDNA derived from
N_Geneseq_36:T96002  +  234.00  297.07  6.0e-09   1374  ! Human cytokine-inducible SH2-c
N_Geneseq_36:V38661  +  229.50  287.29  2.1e-08   2187  ! Mus musculus SOCS3 gene. Suppr
N_Geneseq_36:V34188  +  221.00  275.60  9.5e-08   2378  ! Human secreted protein gene 35
N_Geneseq_36:V38681  +  147.50  189.47  0.0059     848  ! Homo sapiens SOCS11 gene. Suppr
N_Geneseq_36:V38668  +  145.00  183.13  0.0134    1221  ! Homo sapiens SOCS5 gene. Suppr
N_Geneseq_36:V38687  +  138.50  168.83  0.0838    2438  ! Mus musculus SOCS14 cDNA. Supp
N_Geneseq_36:V71075  +  126.50  153.01  0.6374    2532  ! Green fluorescent protein-prot
N_Geneseq_36:V38667  +  126.00  152.35  0.6939    2537  ! Mus musculus SOCS5 gene. Suppr
N_Geneseq_36:Q21065  +  121.00  129.64  12.77     17041  ! Genomic DNA of human PACAP 38
N_Geneseq_36:Q67057  +  121.00  129.64  12.77     17041  ! PACPAP38 DNA. PACAP38 gene pr
N_Geneseq_36:V71026  +  119.50  142.79  2.36      2907  ! p85alpha-green flourescent prc
N_Geneseq_36:V71035  +  119.50  142.77  2.37      2913  ! p85alpha-green flourescent prc
N_Geneseq_36:Q27254  +  119.50  141.53  2.78      3372  ! Growth Factor Receptor Bound p
N_Geneseq_36:T03198  +  119.50  141.53  2.78      3372  ! Human GRB-1 genomic DNA sequen
N_Geneseq_36:T35308  +  118.50  145.85  1.60      1747  ! Rat M1PTP gene cDNA clone deri
N_Geneseq_36:T12235  +  118.50  135.70  5.87      5737  ! pp60PIK cDNA. pp60PIK peptide
N_Geneseq_36:V38677  -  116.50  141.37  2.84      2180  ! Homo sapiens SOCS9 gene. Suppr
N_Geneseq_36:T80413  +  116.50  115.87  74.67     43280  ! Tylactone synthase gene clust
N_Geneseq_36:X39794  +  116.00  149.68  0.9778     764  ! Gastric cancer associated gene.
N_Geneseq_36:V71076  +  113.50  136.12  5.56      2562  ! Protein tyrosine phosphatase 1
N_Geneseq_36:Q46806  -  109.50  109.99  158.71    29879  ! eryA region of S. erythraea c
N_Geneseq_36:T43076  +  109.00  128.10  15.56     3319  ! Wheat acetyl-CoA carboxylase A
N_Geneseq_36:V33412  +  109.00  128.10  15.56     3319  ! 5' end flanking sequence of wh
N_Geneseq_36:V09214  +  107.00  130.36  11.64     1881  ! Crkl cDNA sequence. Use of ant
N_Geneseq_36:Q06844  +  107.00  128.75  14.31     2271  ! Amylase gene from Streptomyces
N_Geneseq_36:Q29515  -  107.00  125.36  22.12     3382  ! Bovine herpes virus type 1 gly
N_Geneseq_36:Q48249  -  107.00  125.36  22.12     3382  ! Bovine herpesvirus type I gI g
N_Geneseq_36:Q67058  +  105.50  137.40  4.72      657  ! PACPAP38 promoter. PACAP38 gene
N_Geneseq_36:V09005  -  105.50  114.99  83.57     9077  ! Vector containing Rabbit TGFbe
N_Geneseq_36:V09006  -  105.50  114.99  83.57     9077  ! Vector containing human TGFbet
N_Geneseq_36:T35310  +  104.50  128.39  15.00     1624  ! Human SH-PTP1 cDNA clone deriv
N_Geneseq_36:T35306  +  104.50  126.01  20.34     2145  ! Human SH-PTP1 gene (protein ty
N_Geneseq_36:N80309  +  103.00  123.51  28.02     2291  ! Entire amylase gene. Expressid
N_Geneseq_36:T97129  +  102.50  124.70  24.06     1848  ! Human netrin-1 cDNA. Human
N_Geneseq_36:V21187  +  102.50   95.93  963.02    53789  ! Amycolatopsis mediterranei
N_Geneseq_36:V34002  +  102.00  126.42  19.30     1401  ! S. peucetius dnrX gene. Pro
N_Geneseq_36:V69308  +  101.00  121.63  35.68     2111  ! Human EPRG1 cDNA #2. New EP

seq_name: N_Geneseq_36:V38659

seq_documentation_block:
ID   V38659 standard; DNA; 1235 BP.
AC   V38659;
DT   27-OCT-1998  (first entry)
DE   Mus musculus SOCS1 gene.
KW   SOCS; suppressor of cytokine signalling; PCR primer;
KW   autoimmune disease; diagnosis; cancer; treatment;
KW   cytokine mediated cellular responsiveness; hyperimmunity;
KW   immunosuppression; allergies; hypertension; ss.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   CDS             161. .799
FT                   /*tag=  a
FT                   /product= SOCS1 protein
PN   WO9820023-A1.
PD   14-MAY-1998.
PF   31-OCT-1997; AU0729.
PR   14-FEB-1997; AU-005117.
PR   01-NOV-1996; AU-003384.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Alexander WS, Hilton DJ, Metcalf D, Nicholson SE,
PI   Nicola NA, Richardson RT, Starr R, Viney EM, Willson TA;
DR   WPI; 98-286854/25.
DR   P-PSDB; W62613.
PT   Suppressor of cytokine signalling proteins - useful to treat
PT   disease, injury or abnormality involving cytokine mediated cellular
PT   responsiveness e.g. hyperimmunity, immunosuppression, allergies and
PT   hypertension
PS   Claim 14; Page 108-109; 325pp; English.
CC   The sequence is that of a gene encoding a suppressor of cytokine
CC   signalling protein (SOCS). SOCS can be used to screen for naturally
CC   occurring antibodies to SOCS, which may occur, e.g. in some autoimmune
CC   diseases. Alternatively, specific antibodies can be used to
CC   screen for SOCS, which is useful as a knowledge of SOCS levels
CC   may be important for the diagnosis of certain cancers. Soluble
CC   SOCS polypeptides can be used to treat disease, injury or
CC   abnormality involving cytokine mediated cellular responsiveness,
CC   e.g. hyperimmunity, immunosuppression, allergies and hypertension.
SQ   Sequence   1235 BP;    192 A;    421 C;    347 G;    275 T;


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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-08-962-560A-4 x V38659   ..

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     161 ATGGTAGCACGCAACCAGGTGGCAGCCGACAATGCGATCTCCCCGGCAGC 210

      17 aGluProArgArgArgSerGluProSerSerSerSerSerSerSerSerP 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     211 AGAGCCCCGACGGCGGTCAGAGCCCTCCTCGTCCTCGTCTTCGTCCTCGC 260

      34 roAlaAlaProValArgProArgProCysProAlaValProAlaProAla 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     261 CAGCGGCCCCCGTGCGTCCCCGGCCCTGCCCGGCGGTCCCAGCCCCAGCC 310

      51 ProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArgAr 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     311 CCTGGCGACACTCACTTCCGCACCTTCCGCTCCCACTCCGATTACCGGCG 360
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     67 gIleThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTyrTrpGlyP 84
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    361 CATCACGCGGACCAGCGCGCTCCTGGACGCCTGCGGCTTCTATTGGGGAC 410

     84 roLeuSerValHisGlyAlaHisGluArgLeuArgAlaGluProValGly 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    411 CCCTGAGCGTGCACGGGGCGCACGAGCGGCTGCGTGCCGAGCCCGTGGGC 460

    101 ThrPheLeuValArgAspSerArgGlnArgAsnCysPhePheAlaLeuSe 117
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    461 ACCTTCTTGGTGCGCGACAGTCGTCAACGGAACTGCTTCTTCGCGCTCAG 510

    117 rValLysMetAlaSerGlyProThrSerIleArgValHisPheGlnAlaG 134
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    511 CGTGAAGATGGCTTCGGGCCCCACGAGCATCCGCGTGCACTTCCAGGCCG 560

    134 lyArgPheHisLeuAspGlySerArgGluThrPheAspCysLeuPheGlu 150
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    561 GCCGCTTCCACTTGGACGGCAGCCGCGAGACCTTCGACTGCCTTTTCGAG 610

    151 LeuLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAlaProLe 167
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    611 CTGCTGGAGCACTACGTGGCGGCGCCGCGCCGCATGTTGGGGGCCCCGCT 660

    167 uArgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleV 184
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    661 GCGCCAGCGCCGCGTGCGGCCGCTGCAGGAGCTGTGTCGCCAGCGCATCG 710

    184 alAlaAlaValGlyArgGluAsnLeuAlaArgIleProLeuAsnProVal 200
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    711 TGGCCGCCGTGGGTCGCGAGAACCTGGCGCGCATCCCTCTTAACCCGGTA 760

    201 LeuArgAspTyrLeuSerSerPheProPheGlnIle 212
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seq_name: N_Geneseq_36:V42701

seq_documentation_block:
ID V42701 standard; cDNA; 1087 BP.
AC V42701;
DT 30-OCT-1998 (first entry)
DE cDNA encoding a STAT function regulatory protein designated SIIS-1.
KW SIIS-1; STAT-induced inhibitor; STAT function;
KW JAK/STAT signal transmission system; STAT3; STAT6; inhibit;
KW tyrosine phosphorylation; gp130; cytokine-regulating protein; CIS;
KW screen; cytokine regulatory; inhibitory activity; ds.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 16. .654
FT /*tag= a
PN WO9830688-A1.
PD 16-JUL-1998.
PF 23-OCT-1997; J03860.
PR 10-JAN-1997; JP-014737.
PA (KISH/) KISHIMOTO T.
PI Naka T;
DR WPI; 98-399137/34.
DR P-PSDB; W70962.
PT STAT function regulatory protein - used in screening candidate
PT substances for cytokine regulatory activity
PS Claim 5; Pages 39-41; 60pp; Japanese.
CC The present sequence encodes a protein (designated SIIS-1, STAT-induced
CC inhibitor of STAT function 1) which regulates STAT protein function in
CC the JAK/STAT signal transmission system in mammalian cells. The protein
CC is induced by STAT3 or STAT6. It inhibits tyrosine phosphorylation of
CC STAT3 and of gp130. The SIIS-1 protein sequence contains an SH2 domain
CC and is related to the cytokine-regulating protein CIS. SIIS-1, or
CC transformant cells expressing it, may be used to screen candidate
CC substances for cytokine regulatory or inhibitory activity.
SQ Sequence 1087 BP; 171 A; 363 C; 305 G; 248 T;

alignment_scores:
Quality: 1093.00 Length: 212
Ratio: 5.180 Gaps: 0
Percent Similarity: 99.528 Percent Identity: 98.585

alignment_block:
US-08-962-560A-4 x V42701 ..

Align seg 1/1 to: V42701 from: 1 to: 1087

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     17 aGluProArgArgArgSerGluProSerSerSerSerSerSerSerSerP 34
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     66 AGAGCCCCGACGGCGGTCAGAGCCCTCCTCGTCCTCGTCTTCGTCCTCGC 115

     34 roAlaAlaProValArgProArgProCysProAlaValProAlaProAla 50
        ||||||||||||||||||||||||||||||:::|||||||||||||||||
    116 CAGCGGCCCCCGTGCGTCCCCGGCCCTGCCCGGGGGTCCCAGCCCCAGCC 165

     51 ProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArgAr 67
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    166 CCTGGCGACACTCACTTCCGCACCTTCCGCTCCCACTCCGATTACCGGCG 215

     67 gIleThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTyrTrpGlyP 84
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    216 CATCACGCGGACCAGCGCGCTCCTGGACGCCTGCGGCTTCTATTGGGGAC 265

     84 roLeuSerValHisGlyAlaHisGluArgLeuArgAlaGluProValGly 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    266 CCCTGAGCGTGCACGGGGCGCACGAGCGGCTGCGTGCCGAGCCCGTGGGC 315

    101 ThrPheLeuValArgAspSerArgGlnArgAsnCysPhePheAlaLeuSe 117
        |||||||||||||||||||||||||||||  ||||||||||||||||||
    316 ACCTTCTTGGTGCGCGACAGTCGCCAACCGAACTGCTTCTTCGCGCTCAG 365

    117 rValLysMetAlaSerGlyProThrSerIleArgValHisPheGlnAlaG 134
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    366 CGTGAAGATGGCTTCGGGCCCCACGAGCATCCGCGTGCACTTCCAGGCCG 415

    134 lyArgPheHisLeuAspGlySerArgGluThrPheAspCysLeuPheGlu 150
        ||||||||||||||||||||:::|||||||||||||||||||||||||||
    416 GCCGCTTCCACTTGGACGGCAACCGCGAGACCTTCGACTGCCTTTTCGAG 465

    151 LeuLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAlaProLe 167
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    466 CTGCTGGAGCACTACGTGGCGGCGCCGCGCCGCATGTTGGGGGCCCCGCT 515

    167 uArgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleV 184
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    516 GCGCCAGCGCCGCGTGCGGCCGCTGCAGGAGCTGTGTCGCCAGCGCATCG 565

    184 alAlaAlaValGlyArgGluAsnLeuAlaArgIleProLeuAsnProVal 200
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    566 TGGCCGCCGTGGGTCGCGAGAACCTGGCGCGCATCCCTCTTAACCCGGTA 615

    201 LeuArgAspTyrLeuSerSerPheProPheGlnIle 212
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seq_name: N_Geneseq_36:V38663

seq_documentation_block:
ID V38663 standard; DNA; 2807 BP.
AC V38663;
DT 27-OCT-1998 (first entry)
DE Rattus norvegicus SOCS1 gene.
KW SOCS; suppressor of cytokine signalling; PCR primer;
KW autoimmune disease; diagnosis; cancer; treatment;
KW cytokine mediated cellular responsiveness; hyperimmunity;

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KW   immunosuppression; allergies; hypertension; ss.
OS   Rattus norvegicus.
FH   Key             Location/Qualifiers
FT   CDS             1739. .2377
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FT                   /product= SOCS1 protein
PN   WO9820023-A1.
PD   14-MAY-1998.
PF   31-OCT-1997; AU0729.
PR   14-FEB-1997; AU-005117.
PR   01-NOV-1996; AU-003384.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Alexander WS, Hilton DJ, Metcalf D, Nicholson SE,
PI   Nicola NA, Richardson RT, Starr R, Viney EM, Willson TA;
DR   WPI; 98-286854/25.
DR   P-PSDB; W62617.
PT   Suppressor of cytokine signalling proteins - useful to treat
PT   disease, injury or abnormality involving cytokine mediated cellular
PT   responsiveness e.g. hyperimmunity, immunosuppression, allergies and
PT   hypertension
PS   Claim 14; Page 117-118; 325pp; English.
CC   The sequence is that of a gene encoding a suppressor of cytokine
CC   signalling protein (SOCS). SOCS can be used to screen for naturally
CC   occurring antibodies to SOCS, which may occur, e.g. in some autoimmune
CC   diseases. Alternatively, specific antibodies can be used to
CC   screen for SOCS, which is useful as a knowledge of SOCS levels
CC   may be important for the diagnosis of certain cancers. Soluble
CC   SOCS polypeptides can be used to treat disease, injury or
CC   abnormality involving cytokine mediated cellular responsiveness,
CC   e.g. hyperimmunity, immunosuppression, allergies and hypertension.
SQ   Sequence   2807 BP;    507 A;    906 C;    899 G;    495 T;


alignment_scores:
           Quality: 1073.00            Length:    212
             Ratio:  5.134              Gaps:      0
 Percent Similarity:  98.585   Percent Identity: 96.226

alignment_block:
 US-08-962-560A-4 x V38663   ..

 Align seg 1/1  to: V38663  from: 1  to: 2807

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         :|||||||||||||||   ||||||||||||||||||||||||||||||
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      34 roAlaAlaProValArgProArgProCysProAlaValProAlaProAla 50
         ||||||||||:::|||||||||||||||||:::|||||||||||||||||
    1839 CGGCGGCCCCGGCGCGTCCCCGGCCCTGCCCGGTGGTCCCGGCCCCGGCT 1888

      51 ProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArgAr 67
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      67 gIleThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTyrTrpGlyP 84
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     134 lyArgPheHisLeuAspGlySerArgGluThrPheAspCysLeuPheGlu 150
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seq_name: N_Geneseq_36:V38662

seq_documentation_block:
ID   V38662 standard; DNA; 1094 BP.
AC   V38662;
DT   27-OCT-1998  (first entry)
DE   Homo sapiens SOCS1 gene.
KW   SOCS; suppressor of cytokine signalling; PCR primer;
KW   autoimmune disease; diagnosis; cancer; treatment;
KW   cytokine mediated cellular responsiveness; hyperimmunity;
KW   immunosuppression; allergies; hypertension; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             24. .659
FT                   /*tag= a
FT                   /product= SOCS1 protein
PN   WO9820023-A1.
PD   14-MAY-1998.
PF   31-OCT-1997; AU0729.
PR   14-FEB-1997; AU-005117.
PR   01-NOV-1996; AU-003384.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Alexander WS, Hilton DJ, Metcalf D, Nicholson SE,
PI   Nicola NA, Richardson RT, Starr R, Viney EM, Willson TA;
DR   WPI; 98-286854/25.
DR   P-PSDB; W62616.
PT   Suppressor of cytokine signalling proteins - useful to treat
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CC   The sequence is that of a gene encoding a suppressor of cytokine
CC   signalling protein (SOCS). SOCS can be used to screen for naturally
CC   occurring antibodies to SOCS, which may occur, e.g. in some autoimmune
CC   diseases. Alternatively, specific antibodies can be used to
CC   screen for SOCS, which is useful as a knowledge of SOCS levels
CC   may be important for the diagnosis of certain cancers. Soluble
CC   SOCS polypeptides can be used to treat disease, injury or
CC   abnormality involving cytokine mediated cellular responsiveness,
CC   e.g. hyperimmunity, immunosuppression, allergies and hypertension.
SQ   Sequence   1094 BP;    167 A;    381 C;    313 G;    233 T;


alignment_scores:
           Quality: 1053.50            Length:    212
             Ratio:  5.041              Gaps:      1
 Percent Similarity:  98.585   Percent Identity: 95.283

alignment_block:
 US-08-962-560A-4 x V38662   ..
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Align seq 1/1  to: V38662  from: 1  to: 1094

      1 MetValAlaArgAsnGlnValAlaAlaAspAsnAlaIleSerProAlaAl 17
        ||||||||||:::|||||||||||||||||||||||||||:::|||   |||||
     24 ATGGTAGCACACAACCAGGTGGCAGCCGACAATGCAGTCTCCACAGCAGC 73

     17 aGluProArgArgArgSerGluProSerSerSerSerSerSerSerSerP 34
        ||||||||||||||   ||||||   ||||||||||||||||||||||
     74 AGAGCCCCGACGGCGGCCAGAACCT...TCCTCCTCTTCCTCCTCCTCGC 120

     34 roAlaAlaProValArgProArgProCysProAlaValProAlaProAla 50
        ||||||||||||:::|||||||||||||||||||||||||||||||||||
    121 CCGCGGCCCCCGCGCGCCCGCGGCCGTGCCCCGCGGTCCCGGCCCCGGCC 170

     51 ProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArgAr 67
        ||||||||||||||||||||||||||||||||||:::|||||||||||
    171 CCCGGCGACACGCACTTCCGCACATTCCGTTCGCACGCCGATTACCGGCG 220

     67 gIleThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTyrTrpGlyP 84
        ||||||||||:::||||||||||||||||||||||||||||||||||||
    221 CATCACGCGCGCCAGCGCGCTCCTGGACGCCTGCGGATTCTACTGGGGGC 270

     84 roLeuSerValHisGlyAlaHisGluArgLeuArgAlaGluProValGly 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    271 CCCTGAGCGTGCACGGGGCGCACGAGCGGCTGCGCGCCGAGCCCGTGGGC 320

    101 ThrPheLeuValArgAspSerArgGlnArgAsnCysPhePheAlaLeuSe 117
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    321 ACCTTCCTGGTGCGCGACAGCCGCCAGCGGAACTGCTTTTTCGCCCTTAG 370

    117 rValLysMetAlaSerGlyProThrSerIleArgValHisPheGlnAlaG 134
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    371 CGTGAAGATGGCCTCGGGACCCACGAGCATCCGCGTGCACTTTCAGGCCG 420

    134 lyArgPheHisLeuAspGlySerArgGluThrPheAspCysLeuPheGlu 150
        ||||||||||||||||||||||||||||:::||||||||||||||||||
    421 GCCGCTTTCACCTGGATGGCAGCCGCGAGAGCTTCGACTGCCTCTTCGAG 470

    151 LeuLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAlaProLe 167
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    471 CTGCTGGAGCACTACGTGGCGGCGCCGCGCCGCATGCTGGGGGCCCCGCT 520

    167 uArgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleV 184
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    521 GCGCCAGCGCCGCGTGCGGCCGCTGCAGGAGCTGTGCCGCCAGCGCATCG 570

    184 alAlaAlaValGlyArgGluAsnLeuAlaArgIleProLeuAsnProVal 200
        |||||:::||||||||||||||||||||||||||||||||||||||||||
    571 TGGCCACCGTGGGCCGCGAGAACCTGGCTCGCATCCCCCTCAACCCCGTC 620

    201 LeuArgAspTyrLeuSerSerPheProPheGlnIle 212
        |||||||||||||||||||||||||||||||||||
    621 CTCCGCGACTACCTGAGCTCCTTCCCCTTCCAGATT 656

seq_name: N_Geneseq_36:T43380

seq_documentation_block:
ID   T43380 standard; cDNA; 1960 BP.
AC   T43380;
DT   11-MAR-1997  (first entry)
DE   Human cytokine response gene CR5.
KW   Cytokine response gene; CR5; interleukin-2; IL-2;
KW   ligand-stimulated gene expression; diagnosis; therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             112. .888
FT                   /*tag=  a
PN   WO9639427-A1.
PD   12-DEC-1996.
PF   05-JUN-1996; U09194.
PR   05-JUN-1995; US-461379.
PR   05-JUN-1995; US-465585.
PR   05-JUN-1995; US-462337.
PR   05-JUN-1995; US-463081.
PR   05-JUN-1995; US-462390.
PR   05-JUN-1995; US-463074.
PA   (DART-) DARTMOUTH COLLEGE.
PI   Beadling C,  Smith KA;
DR   WPI; 97-043062/04.
DR   P-PSDB; W08137.
PT   Cytokine response proteins and genes - used in the detection and
PT   therapy of diseases caused by a mutation in the CR coding region
PS   Disclosure; Page 25-27; 81pp; English.
CC   8 Clones (T43376-83) contg. interleukin-2 (IL-2)-induced genes were
CC   isolated from a human IL2 receptor-positive T blast cell cDNA
CC   library following IL-2 stimulation.  6 Of these ligand-induced genes
CC   (CR1, 2, 3, 5, 6, 8) are novel.  The CR5 gene encodes a 28 kDa
CC   protein (W08137) that shows homology to src homology 2 (SH2)
CC   domains.  CR5 expression is markedly induced during IL2-promoted
CC   T-cell proliferation.  CR genes and polypeptides (W08133-40) are
CC   useful as diagnostic or therapeutic agents; CR gene sequences can
CC   be used to detect and treat allelic mutations.
SQ   Sequence   1960 BP;    402 A;    622 C;    523 G;    413 T;


alignment_scores:
           Quality:  249.50              Length:    297
             Ratio:  1.835                 Gaps:     10
 Percent Similarity:  45.791   Percent Identity: 27.946

alignment_block:
 US-08-962-560A-4 x T43380   ..

 Align seq 1/1  to: T43380  from: 1  to: 1960

     14 SerProAlaAlaGluProArgArgArgSerGluProSerSerSerSerSe 30
        :::|||:::|||   |||   |||      :::|||          |||||
     10 GCCCCGGGAGCCTACCCAGCACGCGCTCCGCGCCCACTGGTTCCCTCCAG 59

     30 rSerSerSerProAla...AlaProValArg..................... 39
        |         ||||||   :::|||:::|||
     60 CCGCCGCCGTCCAGCCGAGTCCCCACTCCGGAGTCGCCGCTGCCGCGGGG 109

     40 .....................ProArgProCysProAlaVal...... 46
                             |||||||||      ||||||
    110 ACATGGTCCTCTGCGTTCAGGGACCTCGTCCTTTGCTGGCTGTGGAGCGG 159

     46 ..................................................... 46

    160 ACTGGGCAGCGGCCCCTGTGGGCCCCGTCCCTGGAACTGCCCAAGCCAGT 209

     47 .............ProAla.............................. 48
                     ||||||
    210 CATGCAGCCCTTGCCTGCTGGGGCCTTCCTCGAGGAGGTGGCAGAGGGTA 259

     49 ..ProAlaProGlyAspThrHisPheArgThrPheArgSerHisSerAsp 64
          ||||||      :::::::::   :::::::::      :::::::|||
    260 CCCCAGCCCAGACAGAGAGTGAGCCAAAGGTGCTGGACCCAGAGGAGGAT 309

     65 TyrArgArgIleThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTy 81
                |||:::::::|||   :::   |||         |||:::||
    310 CTGCTGTGCATAGCCAAGACCTTCTCCTACCTTCGGGAATCTGGCTGGTA 359

     81 rTrpGlyProLeuSerValHisGlyAlaHisGluArgLeuArgAlaGluP 98
        |||||||   :::::::::      |||:::::::::|||:::      |
    360 TTGGGGTTCCATTACGGCCAGCGAGGCCCGACAACACCTGCAGAAGATGC 409

     98 roValGlyThrPheLeuValArgAspSerArgGlnArgAsnCysPhePhe 114
        ||  ||||||||||||||||||||||   :::   :::   :::|||
    410 CAGAAGGCACGTTCTTAGTACGTGACAGCACGCACCCCAGCTACCTGTTC 459

    115 AlaLeuSerValLysMetAlaSerGlyProThrSerIleArgValHisPh 131
        :::||||||||||||   :::   |||||||||:::::|||:::::::::
    460 ACGCTGTCAGTGAAAACCACTCGTGGCCCCACCAATGTACGCATTGAGTA 509

    131 eGlnAlaGlyArgPheHisLeuAspGly.........SerArgGlu.... 143
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     :      :::   |||:::||||||:::         ||||||
510 TGCCGACTCCAGCTTCCGTCTGGACTCCAACTGCTTGTCCAGGCCACGCA 559

144 .....ThrPheAspCysLeuPheGluLeuLeuGluHisTyrValAla... 157
        :::|||     :::   :::|||:::::::||||||||||||
560 TCCTGGCCTTTCCGGATGTGGTCAGCCTTGTGCAGCACTATGTGGCCTCC 609

158 ..................................AlaProArgArgMe 162
                                     ||||||
610 TGCACTGCTGATACCCGAAGCGACAGCCCCGATCCTGCTCCCACCCCGGC 659

162 tLeuGlyAlaPro..................................... 166
     |||      |||
660 CCTGCCTATGCCTAAGGAGGATGCGCCTAGTGACCCAGCACTGCCTGCTC 709

167 ..........................................LeuArg 168
                                               :::|||
710 CTCCACCAGCCACTGCTGTACACCTAAAACTGGTGCAGCCCTTTGTACGC 759

169 GlnArgArgValArgProLeuGlnGluLeuCysArg.........GlnAr 182
    :::|||   :::|||   ||||||:::||||||||         :::||
760 AGAAGAAGTGCCCGCAGCCTGCAACACCTGTGCCGCCTTGTCATCAACCG 809

182 gIleValAlaAlaValGlyArgGluAsnLeuAlaArgIleProLeuAsnP 199
    |:::||||||   |||                  :::||||||
810 TCTGGTGGCCGACGTGGAC..............TGCCTGCCACTGCCCC 844

199 roValLeuArgAspTyrLeuSerSerPheProPheGlnIle 212
        :::   |||||||||   ::::::|||||||||:::
845 GGCGCATGGCCGACTACCTCCGACAGTACCCCTTCCAGCTC 885

seq_name: N_Geneseq_36:V38660

seq_documentation_block:
ID   V38660 standard; DNA; 1121 BP.
AC   V38660;
DT   27-OCT-1998  (first entry)
DE   Mus musculus SOCS2 gene.
KW   SOCS; suppressor of cytokine signalling; PCR primer;
KW   autoimmune disease; diagnosis; cancer; treatment;
KW   cytokine mediated cellular responsiveness; hyperimmunity;
KW   immunosuppression; allergies; hypertension; ss.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   CDS             223. .819
FT                   /*tag= a
FT                   /product= SOCS2 protein
PN   WO9820023-A1.
PD   14-MAY-1998.
PF   31-OCT-1997; AU0729.
PR   14-FEB-1997; AU-005117.
PR   01-NOV-1996; AU-003384.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Alexander WS, Hilton DJ, Metcalf D, Nicholson SE,
PI   Nicola NA, Richardson RT, Starr R, Viney EM, Willson TA;
DR   WPI; 98-286854/25.
DR   P-PSDB; W62614.
PT   Suppressor of cytokine signalling proteins - useful to treat
PT   disease, injury or abnormality involving cytokine mediated cellular
PT   responsiveness e.g. hyperimmunity, immunosuppression, allergies and
PT   hypertension
PS   Claim 14; Page 111-112; 325pp; English.
CC   The sequence is that of a gene encoding a suppressor of cytokine
CC   signalling protein (SOCS). SOCS can be used to screen for naturally
CC   occurring antibodies to SOCS, which may occur, e.g. in some autoimmune
CC   diseases. Alternatively, specific antibodies can be used to
CC   screen for SOCS, which is useful as a knowledge of SOCS levels
CC   may be important for the diagnosis of certain cancers. Soluble
CC   SOCS polypeptides can be used to treat disease, injury or
CC   abnormality involving cytokine mediated cellular responsiveness,
CC   e.g. hyperimmunity, immunosuppression, allergies and hypertension.
SQ   Sequence   1121 BP;    317 A;    274 C;    263 G;    267 T;

alignment_scores:
            Quality:  234.50              Length:    248
              Ratio:  1.777                 Gaps:      9
 Percent Similarity:  53.226   Percent Identity: 29.032

alignment_block:
 US-08-962-560A-4 x V38660   ..

 Align seg 1/1  to: V38660  from: 1  to: 1121

     14 SerProAlaAlaGluProArgArgArgSerGluProSerSerSer..... 28
        ||||||        |||     |||:::     :::   |||
     85 TCCCCTCCCCCTCCGCCACCATTTCGGACACCCTGCACACTCTCGTTTTG 134

     29 ...................SerSerSerSerSerProAlaAlaProValA 39
                            :::|||:::   :::|||   ||||||:::|
    135 GGGTACCCTGTGACTTCCAGGCAGCACGCGAGGTCCACTGGCCCCAGCTC 184

     39 rgProArgProCysProAlaValProAlaProAlaPro............ 51
        ||        |||   :::             :::|||
    185 GGGCGACCAGCTGTCTGGGACGTGTTGACTCATCTCCCATGACCCTGCGG 234

     52 ..............GlyAspThrHisPheArgThrPheArgSerHis.. 62
                       |||:::         ||||||   ||||||:::
    235 TGCCTGGAGCCCTCCGGGAATGGAGCGGACAGGACG...CGGAGCCAGTG 281

     63 ..............................SerAspTyrArgArgIleT 69
                                     :::       |||::::
    282 GGGGACCGCGGGGTTGCCGGAGGAACAGTCCCCCGAGGCGGCGCGTCTGG 331

     69 hrArgThrSerAlaLeuLeuAspAlaCysGlyPheTyrTrpGlyProLeu 85
        ::::::::        |||:::     |||:::|||||||||   :::
    332 CGAAAGCCCTGCGCGAGCTCAGTCAAACAGGATGGTACTGGGGAAGTATG 381

     86 SerValHisGlyAlaHisGluArgLeuArgAlaGluProValGlyThrPh 102
        :::|||:::   |||   |||:::|||:::      |||   ||||||||
    382 ACTGTTAATGAAGCCAAAGAGAAATTAAAAGAGGCTCCAGAAGGAACTTT 431

    102 eLeuValArgAspSerArgGlnArgAsnCysPhePheAlaLeuSerValL 119
        ||||:::|||||||||   :::   :::   :::::::::::::|||||||
    432 CTTGATTAGAGATAGTTCGCATTCAGACTACCTACTAACTATATCCGTTA 481

    119 ysMetAlaSerGlyProThrSerIleArgValHisPheGlnAlaGlyArg 135
        ||   ::::::||||||||||:::::::|||::::::::::|||   |||:::
    482 AGACGTCAGCTGGACCGACTAACCTGCGGATTGAGTACCAAGATGGGAAA 531

    136 PheHisLeuAsp.................GlySerArgGluThrPheAs 146
        |||:::||||||                 ::::::   :::   |||||
    532 TTCAGATTGGATTCTATCATATGTGTCAAGTCCAAGCTTAAACAGTTTGA 581

    146 pCysLeuPheGluLeuLeuGluHisTyrVal.................... 156
        |   :::   :::|||::::::::::||||||
    582 CAGTGTGGTTCATCTGATTGACTACTATGTCCAGATGTGCAAGGATAAAC 631

    157 ..........AlaAlaProArgArg..............MetLeuGly 164
                  ||||||||||:::                  |||
    632 GGACAGGCCCAGAAGCCCCACGGAATGGGACTGTTCACCTGTACCTGACC 681

    165 AlaProLeuArgGlnArgArgValArgProLeuGlnGluLeuCysArgGl 181
           ||||||            :::      ||||||::::::||||||
    682 AAACCTCTG...TATACATCAGCACCCACTCTGCAGCATTTCTGTCGACT 728

    181 nArgIleValAlaAlaValGlyArgGluAsnLeuAlaArgIleProLeuA 198
           |||      ::::::|||      ::::::      :::||||||
    729 CGCCATTAACAAATGTACCGGT......ACGATCTGGGGACTGCCTTTAC 772

    198 snProValLeuArgAspTyrLeuSerSerPheProPheGlnIle 212
              |||:::||||||||||:::::::::   |||||||:::
    773 CAACAAGACTAAAAGATTACTTGGAAGAATATAAATTCCAGGTA 816

seq_name: N_Geneseq_36:V69307
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seq_documentation_block:
ID   V69307 standard; cDNA; 2342 BP.
AC   V69307;
DT   01-FEB-1999  (first entry)
DE   Human EPRG1 cDNA #1.
KW   EPRG1; EPO primary response gene 1; diagnosis; gene therapy; immunity;
KW   disease; vaccine; inoculate; antibody; T cell; anaemia; polycythemia;
KW   cancer; neutropenia; AIDS; diabetes, myelosuppression; allergy; asthma;
KW   autoimmune disease; inflammatory disease; chromosome mapping; human; ss.
OS   Homo sapiens.
PN   EP-877030-A2.
PD   11-NOV-1998.
PF   07-MAY-1998; 303597.
PR   01-MAY-1998; US-071342.
PR   07-MAY-1997; US-045890.
PA   (SMIK ) SMITHKLINE BECKMAN CORP.
PI   Dillon S, Lord K;
DR   WPI; 98-570499/49.
DR   P-PSDB; W82504.
PT   New EPO primary response gene polypeptides and polynucleotides -
PT   useful as diagnostic reagents and for prevention and treatment of
PT   cancer and autoimmune and inflammatory diseases
PS   Claim 14; Page 18-19; 25pp; English.
CC   This sequence encodes a novel human EPO primary response gene 1 (EPRG1)
CC   polypeptide. EPRG1 polypeptides and polynucleotides are useful for
CC   diagnosing a disease or susceptibility to a disease by detecting
CC   mutations in the EPRG1 gene using probes containing the EPRG1 nucleotide
CC   sequence, or determining EPRG1 polypeptide or mRNA expression levels
CC   EPRG1 polypeptides can be used to screen for agonists and antagonists
CC   which bind the EPRG1 polypeptide by measuring resulting mRNA levels with
CC   ELISA. These can be used in treatment to activate (agonist) or inhibit
CC   (antagonist eg EPRG1 ligand, receptor or substrate) EPRG1 activity, in
CC   addition to direct administration of antisense sequences to prevent
CC   expression, or EPRG1 polypeptides to treat conditions associated with
CC   a lack of EPRG1 protein. Gene therapy may also be used to affect
CC   endogenous EPRG1 polypeptide production. EPRG1 antibodies are useful for
CC   inducing an immune response to immunise and prevent diseases, and for
CC   isolating EPRG1 clones or purifying the polypeptides by affinity
CC   chromatography. EPRG1 polypeptides can be administered directly or as a
CC   vaccine to inoculate against disease by inducing an antibody and T-cell
CC   response. Diseases diagnosed, prevented or treated include anaemia,
CC   polycythemia, cancer, neutropenia, AIDS, drug-induced anaemia, diabetes,
CC   myelosuppression, autoimmune diseases, rheumatoid arthritis and multiple
CC   sclerosis, and inflammatory diseases, including asthma and allergies. The
CC   EPRG1 polypeptide is also useful for mapping the gene to a chromosome,
CC   allowing gene inheritance to be studied through linkage analysis. The
CC   3'-UTR segment of EPRG1 RNA may be useful to screen for agents which
CC   modulate RNA stability and turnover rate.
SQ   Sequence   2342 BP;    495 A;    685 C;    655 G;    506 T;


alignment_scores:
           Quality:  234.50              Length:    231
             Ratio:  1.804                 Gaps:      9
 Percent Similarity:  56.277   Percent Identity: 29.870

alignment_block:
 US-08-962-560A-4 x V69307   ..

 Align seg 1/1  to: V69307  from: 1  to: 2342

      30 SerSerSerSerProAlaAlaProValArgProArgProCysProAlaVa 46
         |||:::   :::|||:::|||   |||              ||||||::
       7 TCCACGCTGGCTCCGTGCGCCATGGTCACCCACAGCAAGTTTCCCGCCGC 56

      46 lProAlaProAlaProGlyAspThrHisPheArg......ThrPheArgS 61
         :            |||   ||||||   :::|||      ||||||   |
      57 CGGGATGAGCCGCCCCCTGGACACCAGCCTGCGCCTCAAGACCTTCAGCT 106

      61 erHisSerAspTyrArgArgIleThrArgThrSerAlaLeuLeuAspAla 77
         ||   |||:::|||:::  ::::::::::::        |||:::
     107 CCAAGAGCGAGTACCAGCTGGTGGTGAACGCAGTGCGCAAGCTGCAGGAG 156

      78 CysGlyPheTyrTrpGlyProLeuSerValHisGlyAlaHisGluArgLe 94
         ||||||||||||:::  ::::::         |||:::      ||
     157 AGCGGCTTCTACTGGAGCGCAGTGACCGGCGGCGAGGCGAACCTGCTGCT 206

      94 uArgAlaGluProValGlyThrPheLeuValArgAspSerArgGlnArgA 111
         |  |||||||||:::|||||||||||||:::|||||||||  :::::::
     207 CAGTGCCGAGCCCGCCGGCACCTTTCTGATCCGCGACAGCTCGGACCAGC 256

     111 snCysPhePheAlaLeuSerValLysMetAlaSerGlyProThrSerIle 127
         ::  ||||||:::||||||||||||      ||||||      ::::::
     257 GCCACTTCTTCACGCTCAGCGTCAAGACCCAGTCTGGGACCAAGAACCTG 306

     128 ArgValHisPheGlnAlaGlyArgPheHisLeuAspGlySer...ArgGl 143
         |||:::::::  ::::::|||  |||  |||:::::::::  |||::
     307 CGCATCCAGTGTGAGGGGGGCAGCTTCTCTCTGCAGAGCGATCCCCGGAG 356

     143 uThr.............PheAspCysLeuPheGluLeuLeuGluHisT 155
         :|||             |||||||||:::::::::|||::::::|||
     357 CACGCAGCCCGTGCCCCGCTTCGACTGCGTGCTCAAGCTGGTGCACCACT 406

     155 yrVal..................................... 156
         ||:::
     407 ACATGCCGCCCCCTGGAGCCCCCTCCTTCCCCTCGCCACCTACTGAACCC 456

     157 .....................................AlaAl 158
                                              :::
     457 TCCTCCGAGGTGCCCGAGCAGCCGTCTGCCCAGCCACTCCCTGGGAGTCC 506

     158 aProArgArg.....................................M 162
          |||||||||                                  :
     507 CCCCAGAAGAGCCTATTACATCTACTCCGGGGGCGAGAAGATCCCCCTGG 556

     162 etLeuGlyAlaProLeuArgGlnArgArgValArgProLeuGlnGluLeu 178
         ::|||:::  ||||||  :::  :::|||      ||||||:::|||
     557 TGTTGAGCCGGCCCCTC...TCCTCCAACGTGGCCACTCTTCAGCATCTC 603

     179 CysArgGlnArgIleValAlaAlaVal...GlyArgGluAsnLeuAlaAr 194
         |||||||:::  :::  :::  :::  :::  |||:::::::::::
     604 TGTCGGAAGACCGTCAACGGCCACCTGGACTCCTATGAGAAAGTCACCCA 653

     194 gIleProLeuAsnProValLeuArgAspTyrLeuSerSerPhe 208
         ::::|||  :::|||:::  |||:::::|||:::::::::
     654 GCTGCCG...GGGCCCATT...CGGGAGTTCCTGGACCAGTAC 690

seq_name: N_Geneseq_36:V69309

seq_documentation_block:
ID   V69309 standard; cDNA; 2342 BP.
AC   V69309;
DT   01-FEB-1999  (first entry)
DE   Human EPRG1 cDNA derived from expressed sequence tags, EST's.
KW   EPRG1; EPO primary response gene 1; diagnosis; gene therapy; immunity;
KW   disease; vaccine; inoculate; antibody; T cell; anaemia; polycythemia;
KW   cancer; neutropenia; AIDS; diabetes, myelosuppression; allergy; asthma;
KW   autoimmune disease; inflammatory disease; chromosome mapping; human;
KW   expressed sequence tag; EST; ss.
OS   Homo sapiens.
PN   EP-877030-A2.
PD   11-NOV-1998.
PF   07-MAY-1998; 303597.
PR   01-MAY-1998; US-071342.
PR   07-MAY-1997; US-045890.
PA   (SMIK ) SMITHKLINE BECKMAN CORP.
PI   Dillon S, Lord K;
DR   WPI; 98-570499/49.
PT   New EPO primary response gene polypeptides and polynucleotides -
PT   useful as diagnostic reagents and for prevention and treatment of
PT   cancer and autoimmune and inflammatory diseases
PS   Claim 13; Page 22-23; 25pp; English.
CC   This sequence encodes a novel human EPO primary response gene 1 (EPRG1)
CC   polypeptide derived from expressed sequence tags (EST's). EPRG1
CC   polypeptides and polynucleotides are useful for diagnosing a disease or
CC   susceptibility to a disease by detecting mutations in the EPRG1 gene
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CC   using probes containing the EPRG1 nucleotide sequence, or determining
CC   EPRG1 polypeptide or mRNA expression levels EPRG1 polypeptides can be
CC   used to screen for agonists and antagonists which bind the EPRG1
CC   polypeptide by measuring resulting mRNA levels with ELISA. These can be
CC   used in treatment to activate (agonist) or inhibit (antagonist eg EPRG1
CC   ligand, receptor or substrate) EPRG1 activity, in addition to direct
CC   administration of antisense sequences to prevent expression, or EPRG1
CC   polypeptides to treat conditions associated with a lack of EPRG1 protein.
CC   Gene therapy may also be used to affect endogenous EPRG1 polypeptide
CC   production. EPRG1 antibodies are useful for inducing an immune response
CC   to immunise and prevent diseases, and for isolating EPRG1 clones or
CC   purifying the polypeptides by affinity chromatography. EPRG1 polypeptides
CC   can be administered directly or as a vaccine to inoculate against disease
CC   by inducing an antibody and T-cell response. Diseases diagnosed,
CC   prevented or treated include anaemia, polycythemia, cancer, neutropenia,
CC   AIDS, drug-induced anaemia, diabetes, myelosuppression, autoimmune
CC   diseases, rheumatoid arthritis and multiple sclerosis, and inflammatory
CC   diseases, including asthma and allergies. The EPRG1 polypeptide is also
CC   useful for mapping the gene to a chromosome, allowing gene inheritance to
CC   be studied through linkage analysis. The 3'-UTR segment of EPRG1 RNA may
CC   be useful to screen for agents which modulate RNA stability and turnover
CC   rate.
SQ   Sequence   2342 BP;    495 A;    685 C;    655 G;    506 T;


alignment_scores:
            Quality:  234.50              Length:    231
              Ratio:  1.804                 Gaps:      9
 Percent Similarity:  56.277   Percent Identity: 29.870

alignment_block:
 US-08-962-560A-4 x V69309   ..

 Align seg 1/1  to: V69309  from: 1  to: 2342

      30 SerSerSerSerProAlaAlaProValArgProArgProCysProAlaVa 46
         |||:::   :::|||:::|||   |||               ||||||::
       7 TCCACGCTGGCTCCGTGCGCCATGGTCACCCACAGCAAGTTTCCCGCCGC 56

      46 lProAlaProAlaProGlyAspThrHisPheArg......ThrPheArgS 61
         :            |||   ||||||   :::|||      ||||||   |
      57 CGGGATGAGCCGCCCCCTGGACACCAGCCTGCGCCTCAAGACCTTCAGCT 106

      61 erHisSerAspTyrArgArgIleThrArgThrSerAlaLeuLeuAspAla 77
         ||   |||::::|||:::   ::::::::::::         |||:::
     107 CCAAGAGCGAGTACCAGCTGGTGGTGAACGCAGTGCGCAAGCTGCAGGAG 156

      78 CysGlyPheTyrTrpGlyProLeuSerValHisGlyAlaHisGluArgLe 94
            ||||||||||||:::   ::::::         |||:::      ||
     157 AGCGGCTTCTACTGGAGCGCAGTGACCGGCGGCGAGGCGAACCTGCTGCT 206

      94 uArgAlaGluProValGlyThrPheLeuValArgAspSerArgGlnArgA 111
         |   |||||||||:::||||||||||||:::|||||||||   :::::::
     207 CAGTGCCGAGCCCGCCGGCACCTTTCTGATCCGCGACAGCTCGGACCAGC 256

     111 snCysPhePheAlaLeuSerValLysMetAlaSerGlyProThrSerIle 127
         ::   ||||||:::||||||||||||      ||||||      ::::::
     257 GCCACTTCTTCACGCTCAGCGTCAAGACCCAGTCTGGGACCAAGAACCTG 306

     128 ArgValHisPheGlnAlaGlyArgPheHisLeuAspGlySer...ArgGl 143
         |||::::::   ::::::|||   |||   |||:::::::::   |||::
     307 CGCATCCAGTGTGAGGGGGGCAGCTTCTCTCTGCAGAGCGATCCCCGGAG 356

     143 uThr..............PheAspCysLeuPheGluLeuLeuGluHisT 155
         :|||              ||||||||:::::::::|||::::::||||
     357 CACGCAGCCCGTGCCCCGCTTCGACTGCGTGCTCAAGCTGGTGCACCACT 406

     155 yrVal..................................................... 156
         ||:::
     407 ACATGCCGCCCCCTGGAGCCCCCTCCTTCCCCTCGCCACCTACTGAACCC 456

     157 ..............................................AlaAl 158
                                                     :::

     457 TCCTCCGAGGTGCCCGAGCAGCCGTCTGCCCAGCCACTCCCTGGGAGTCC 506

     158 aProArgArg.....................................M 162
          |||||||||                                    :
     507 CCCCAGAAGAGCCTATTACATCTACTCCGGGGGCGAGAAGATCCCCCTGG 556

     162 etLeuGlyAlaProLeuArgGlnArgArgValArgProLeuGlnGluLeu 178
         ::|||:::   ||||||   :::   :::|||      ||||||:::|||
     557 TGTTGAGCCGGCCCCTC...TCCTCCAACGTGGCCACTCTTCAGCATCTC 603

     179 CysArgGlnArgIleValAlaAlaVal...GlyArgGluAsnLeuAlaAr 194
         ||||||:::   :::   :::   :::   :::   |||:::::::::::
     604 TGTCGGAAGACCGTCAACGGCCACCTGGACTCCTATGAGAAAGTCACCCA 653

     194 gIleProLeuAsnProValLeuArgAspTyrLeuSerSerPhe 208
         ::::|||   :::|||:::   |||:::::::|||:::::::::
     654 GCTGCCG...GGGCCCATT...CGGGAGTTCCTGGACCAGTAC 690

seq_name: N_Geneseq_36:T96002

seq_documentation_block:
ID   T96002 standard; cDNA; 1374 BP.
AC   T96002;
DT   07-JUL-1998  (first entry)
DE   Human cytokine-inducible SH2-containing (CIS) gene.
KW   Human cytokinine-inducible SH2-containing; CIS; erythroprotein; EPO;
KW   tyrosine-phosphorylated interleukin; (IL)-3; signal transduction;
KW   inhibition; anaemia; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             71. .848
FT                   /*tag= a
FT                   /product= "Human CIS protein"
PN   WO9744347-A1.
PD   27-NOV-1997.
PF   21-MAY-1996; U07477.
PR   21-MAY-1996; WO-U07477.
PA   (HARD ) HARVARD COLLEGE.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PI   Dunnington DD, Frantz JD, Shoelson SE;
DR   WPI; 98-018425/02.
DR   P-PSDB; W38319.
PT   Human cytokine-inducible SH2-containing protein and related DNA -
PT   useful for diagnosis of modulators for treatment of, e.g. anaemia
PS   Claim 1; Pages 34-35; 52pp; English.
CC   This sequence encodes the human cytokinine-inducible SH2-containing
CC   (CIS) protein which binds tyrosine-phosphorylated interleukin
CC   (IL)-3 or erythroprotein (EPO) receptors.  When CIS is over expressed
CC   signal transduction through the receptors is inhibited.  Inactivation
CC   of CIS may enhance signalling through (IL)-3 and EPO receptors.
CC   Specific inhibitors of CIS may be useful in the treatment of anaemia.
CC   Labelled CIS or its functional derivatives can be used in binding
CC   assays to determine modulators of CIS activity.  Conditions associated
CC   with CIS protein deficiency can be diagnosed by assaying for the
CC   presence of the CIS gene.  it can be used to treat conditions related
CC   to insufficient CIS protein function.
SQ   Sequence   1374 BP;    264 A;    446 C;    379 G;    285 T;


alignment_scores:
            Quality:  234.00              Length:    286
              Ratio:  1.759                 Gaps:     10
 Percent Similarity:  46.503   Percent Identity: 26.573

alignment_block:
 US-08-962-560A-4 x T96002   ..

 Align seg 1/1  to: T96002  from: 1  to: 1374

      19 ProArgArgArgSerGluProSerSerSerSerSerSerSerSerProAl 35
         |||:::|||:::   :::|||               :::   :::|||
      18 CCGAAGCGACAGCCCGATCCT..............GCTCCCACTCCGGA 52
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 35 aAlaProValArg.........................ProArgProC 43
     :::|||:::|||                        |||||||||
 53 GTCGCCGCTGCGCGGAGACATGGTCCTCTGCGTTCAGGGACCTCGTCCTT 102

 43 ysProAlaVal..................................... 46
       ||||||
103 TGCTGGCTGTGGAGCGGACTGGGCAGCGGCCCCTGTGGGCCCCGTCCCTG 152

 47 ..............................ProAla.............. 48
                                    ||||||
153 GAACTGTCCAAGCCAGTCATGCAGCCCTTGCCTGCTGGGGCCTTCCTCGA 202

 49 ...................ProAlaProGlyAspThrHisPheArgThrP 59
                        ||||||      :::::::::   :::::::
203 GGAGGTGGCAGAGGGTACCCCAGCCCAGACAGAGAGTGAGCCAAAGGTGC 252

 59 heArgSerHisSerAspTyrArgArgIleThrArgThrSerAlaLeuLeu 75
     ::      :::::::|||          |||::::::::|||   :::   |||
253 TGGACCCAGAGGAGGATCTGCTGTGCATAGCCAAGACCTTCTCCTACCTT 302

 76 AspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAlaHisGl 92
            |||:::|||||||||   :::::::::      |||:::::
303 CGGGAATCTGGCTGGTATTGGGGTTCCATTACGGCCAGCGAGGCCCGACA 352

 92 uArgLeuArgAlaGluProValGlyThrPheLeuValArgAspSerArgG 109
     ::::|||:::      |||   |||||||||||||||||||||||   :
353 ACACCTGCAGAAGATGCCAGAAGGCACGTTCTTAGTACGTGACAGCACGC 402

109 lnArgAsnCysPhePheAlaLeuSerValLysMetAlaSerGlyProThr 125
     ::   :::   :::|||:::|||||||||||||   :::   |||||||||
403 ACCCCAGCTACCTGTTCACGCTGTCAGTGAAAACCACTCGTGGCCCCACC 452

126 SerIleArgValHisPheGlnAlaGlyArgPheHisLeuAspGly..... 140
     ::::::|||:::::::::      :::   |||:::|||||||:::
453 AATGTACGCATTGAGTATGCCGACTCCAGCTTCCGTCTGGACTCCAACTG 502

141 ....SerArgGlu.........ThrPheAspCysLeuPheGluLeuLeuG 153
         ||||||            :::|||     :::   :::|||::::
503 CTTGTCCAGGCCACGCATCCTGGCCTTTCCGGATGTGGTCAGTCTTGTGC 552

153 luHisTyrValAla................................... 157
     ::|||||||||||||
553 AGCACTATGTGGCCTCCTGCACTGCTGATACCCGAAGCGACAGCCCCGAT 602

158 ...AlaProArgArgMetLeuGlyAlaPro..................... 166
        ||||||      :::|||      |||
603 CCTGCTCCCACCCCGGTCCTGCCTATGCCTAAGGAGGATGCGCCTAGTGA 652

166 ................................................... 166

653 CCCAGCACTGCCTGCTCCTCCACCAGCCACTGCTGTACACCTAAAACTGG 702

167 ...........LeuArgGlnArgArgValArgProLeuGlnGluLeuCys 179
                :::|||:::     :::|||   ||||||:::||||||
703 TGCAGCCCTTTGTACGCAGAAGCAGTGCCCGCAGCCTGCAACACCTGTGC 752

180 Arg.........GlnArgIleValAlaAlaValGlyArgGluAsnLeuAl 193
     |||         :::|||:::||||||   |||
753 CGCCTTGTCATCAACCGTCTGGTGGCCGACGTGGAC.............. 788

193 aArgIleProLeuAsnProValLeuArgAspTyrLeuSerSerPheProP 210
       :::||||||         :::   :::||||||   :::::::|||
789 .TGCCTGCCACTGCCCCGGCGCATGGCCAACTACCTCCGACAGTACCCCT 837

210 heGlnIle 212
     |||||:::
838 TCCAGCTC 845
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seq_name: N_Geneseq_36:V38661

seq_documentation_block:
ID V38661 standard; DNA; 2187 BP.
AC V38661;
DT 27-OCT-1998 (first entry)
DE Mus musculus SOCS3 gene.
KW SOCS; suppressor of cytokine signalling; PCR primer;
KW autoimmune disease; diagnosis; cancer; treatment;
KW cytokine mediated cellular responsiveness; hyperimmunity;
KW immunosuppression; allergies; hypertension; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 18. .695
FT /*tag= a
FT /product= SOCS3 protein
PN WO9820023-A1.
PD 14-MAY-1998.
PF 31-OCT-1997; AU0729.
PR 14-FEB-1997; AU-005117.
PR 01-NOV-1996; AU-003384.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Alexander WS, Hilton DJ, Metcalf D, Nicholson SE,
PI Nicola NA, Richardson RT, Starr R, Viney EM, Willson TA;
DR WPI; 98-286854/25.
DR P-PSDB; W62615.
PT Suppressor of cytokine signalling proteins - useful to treat
PT disease, injury or abnormality involving cytokine mediated cellular
PT responsiveness e.g. hyperimmunity, immunosuppression, allergies and
PT hypertension
PS Claim 14; Page 113-114; 325pp; English.
CC The sequence is that of a gene encoding a suppressor of cytokine
CC signalling protein (SOCS). SOCS can be used to screen for naturally
CC occurring antibodies to SOCS, which may occur, e.g. in some autoimmune
CC diseases. Alternatively, specific antibodies can be used to
CC screen for SOCS, which is useful as a knowledge of SOCS levels
CC may be important for the diagnosis of certain cancers. Soluble
CC SOCS polypeptides can be used to treat disease, injury or
CC abnormality involving cytokine mediated cellular responsiveness,
CC e.g. hyperimmunity, immunosuppression, allergies and hypertension.
SQ Sequence 2187 BP; 501 A; 632 C; 600 G; 454 T;

alignment_scores:
Quality: 229.50 Length: 228
Ratio: 1.779 Gaps: 9
Percent Similarity: 56.579 Percent Identity: 29.386

alignment_block:
US-08-962-560A-4 x V38661 ..

Align seg 1/1 to: V38661 from: 1 to: 2187

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 33 SerProAlaAlaProValArgProArgProCysProAlaValProAlaPr 49
     :::|||:::|||   |||               |||||||:::
  6 GCTCCGTGCGCCATGGTCACCCACAGCAAGTTTCCCGCCGCCGGGATGAG 55

 49 oAlaProGlyAspThrHisPheArg......ThrPheArgSerHisSerA 64
        |||   ||||||   :::|||      ||||||   |||   |||:
 56 CCGCCCCCTGGACACCAGCCTGCGCCTCAAGACCTTCAGCTCCAAAAGCG 105

 64 spTyrArgArgIleThrArgThrSerAlaLeuLeuAspAlaCysGlyPhe 80
     ::|||:::   ::::::::::::       |||:::      ||||||
106 AGTACCAGCTGGTGGTGAACGCCGTGCGCAAGCTGCAGGAGAGCGGATTC 155

 81 TyrTrpGlyProLeuSerValHisGlyAlaHisGluArgLeuArgAlaGl 97
     |||||||:::   ::::::         |||:::      |||   |||||
156 TACTGGAGCGCCGTGACCGGCGGCGAGGCGAACCTGCTGCTCAGCGCCGA 205

 97 uProValGlyThrPheLeuValArgAspSerArgGlnArgAsnCysPheP 114
     ||||:::|||||||||||||:::|||||||||   :::::::::   ||||
206 GCCCGCGGGCACCTTTCTTATCCGCGACAGCTCGGACCAGCGCCACTTCT 255

114 heAlaLeuSerValLysMetAlaSerGlyProThrSerIleArgValHis 130
     ||:::||||||||||||      ||||||      ::::::|||::::::
256 TCACGTTGAGCGTCAAGACCCAGTCGGGGACCAAGAACCTACGCATCCAG 305

131 PheGlnAlaGlyArgPheHisLeuAspGlySer...ArgGluThr..... 144
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          :::::::|||   |||   |||:::::::::   |||:::|||
     306 TGTGAGGGGGGCAGCTTTTCGCTGCAGAGTGACCCCCGAAGCACGCAGCC 355

     145 .........PheAspCysLeuPheGluLeuLeuGluHisTyrVal.... 156
                 |||||||||:::::::::|||::::::||||||:::
     356 AGTTCCCCGCTTCGACTGTGTACTCAAGCTGGTGCACCACTACATGCCGC 405

     156 ..................................................... 156

     406 CTCCAGGGACCCCCTCCTTTTCTTTGCCACCCACGGAACCCTCGTCCGAA 455

     157 ...................................AlaAlaProArgAr 161
                                           ::::::|||:::||
     456 GTTCCGGAGCAGCCACCTGCCCAGGCACTCCCCGGGAGTACCCCCAAGAG 505

     161 g.....................................MetLeuGlyA 165
         |                                    :::|||:::
     506 AGCTTACTACATCTATTCTGGGGGCGAGAAGATTCCGCTGGTACTGAGCC 555

     165 laProLeuArgGlnArgArgValArgProLeuGlnGluLeuCysArgGln 181
           ||||||   :::   :::|||      |||||||:::||||||||:::
     556 GACCTCTC...TCCTCCAACGTGGCCACCCTCCAGCATCTTTGTCGGAAG 602

     182 ArgIleValAlaAlaVal...GlyArgGluAsnLeuAlaArgIleProLe 197
            :::   :::   :::   :::   |||:::::::::::::::|||
     603 ACTGTCAACGGCCACCTGGACTCCTATGAGAAAGTGACCCAGCTGCCT.. 650

     197 uAsnProValLeuArgAspTyrLeuSerSerPhe 208
          :::|||:::   |||:::::::|||:::::::::
     651 .GGACCCATT...CGGGAGTTCCTGGATCAGTAT 680
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seq_name: N_Geneseq_36:V34188

seq_documentation_block:
ID   V34188 standard; DNA; 2378 BP.
AC   V34188;
DT   28-JAN-1999  (first entry)
DE   Human secreted protein gene 35 clone HTXAK60.
KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW   immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS   Homo sapiens.
PN   WO9839446-A2.
PD   11-SEP-1998.
PF   06-MAR-1998; U04492.
PR   07-MAR-1997; US-038621.
PR   07-MAR-1997; US-040161.
PR   07-MAR-1997; US-040162.
PR   07-MAR-1997; US-040163.
PR   07-MAR-1997; US-040333.
PR   07-MAR-1997; US-040334.
PR   07-MAR-1997; US-040336.
PR   07-MAR-1997; US-040626.
PR   11-APR-1997; US-043311.
PR   11-APR-1997; US-043312.
PR   11-APR-1997; US-043313.
PR   11-APR-1997; US-043314.
PR   11-APR-1997; US-043315.
PR   11-APR-1997; US-043568.
PR   11-APR-1997; US-043569.
PR   11-APR-1997; US-043576.
PR   11-APR-1997; US-043578.
PR   11-APR-1997; US-043580.
PR   11-APR-1997; US-043669.
PR   11-APR-1997; US-043670.
PR   11-APR-1997; US-043671.
PR   11-APR-1997; US-043672.
PR   11-APR-1997; US-043674.
PR   23-MAY-1997; US-047492.
PR   23-MAY-1997; US-047500.
PR   23-MAY-1997; US-047501.
PR   23-MAY-1997; US-047502.
PR   23-MAY-1997; US-047503.
PR   23-MAY-1997; US-047581.
PR   23-MAY-1997; US-047582.
PR   23-MAY-1997; US-047583.
PR   23-MAY-1997; US-047584.
PR   23-MAY-1997; US-047585.
PR   23-MAY-1997; US-047586.
PR   23-MAY-1997; US-047587.
PR   23-MAY-1997; US-047588.
PR   23-MAY-1997; US-047589.
PR   23-MAY-1997; US-047590.
PR   23-MAY-1997; US-047592.
PR   23-MAY-1997; US-047593.
PR   23-MAY-1997; US-047594.
PR   23-MAY-1997; US-047595.
PR   23-MAY-1997; US-047596.
PR   23-MAY-1997; US-047597.
PR   23-MAY-1997; US-047598.
PR   23-MAY-1997; US-047599.
PR   23-MAY-1997; US-047600.
PR   23-MAY-1997; US-047601.
PR   23-MAY-1997; US-047612.
PR   23-MAY-1997; US-047613.
PR   23-MAY-1997; US-047614.
PR   23-MAY-1997; US-047615.
PR   23-MAY-1997; US-047617.
PR   23-MAY-1997; US-047618.
PR   23-MAY-1997; US-047632.
PR   23-MAY-1997; US-047633.
PR   06-JUN-1997; US-048964.
PR   06-JUN-1997; US-048974.
PR   22-AUG-1997; US-056630.
PR   22-AUG-1997; US-056631.
PR   22-AUG-1997; US-056632.
PR   22-AUG-1997; US-056636.
PR   22-AUG-1997; US-056637.
PR   22-AUG-1997; US-056662.
PR   22-AUG-1997; US-056664.
PR   22-AUG-1997; US-056845.
PR   22-AUG-1997; US-056862.
PR   22-AUG-1997; US-056864.
PR   22-AUG-1997; US-056872.
PR   22-AUG-1997; US-056874.
PR   22-AUG-1997; US-056875.
PR   22-AUG-1997; US-056876.
PR   22-AUG-1997; US-056877.
PR   22-AUG-1997; US-056878.
PR   22-AUG-1997; US-056879.
PR   22-AUG-1997; US-056880.
PR   22-AUG-1997; US-056881.
PR   22-AUG-1997; US-056882.
PR   22-AUG-1997; US-056884.
PR   22-AUG-1997; US-056886.
PR   22-AUG-1997; US-056887.
PR   22-AUG-1997; US-056888.
PR   22-AUG-1997; US-056889.
PR   22-AUG-1997; US-056892.
PR   22-AUG-1997; US-056893.
PR   22-AUG-1997; US-056894.
PR   22-AUG-1997; US-056903.
PR   22-AUG-1997; US-056908.
PR   22-AUG-1997; US-056909.
PR   22-AUG-1997; US-056910.
PR   22-AUG-1997; US-056911.
PR   05-SEP-1997; US-057650.
PR   05-SEP-1997; US-057761.
PA   (HUMA-) HUMAN GENOME SCI INC.
PI   Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,
PI   Feng P, Ferrie AM, Fischer CL, Graves KA, Greene JM, Hu JS,
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PI   Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,
PI   Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
DR   WPI; 98-609887/51.
DR   P-PSDB; W75091.
PT   New isolated human genes and the secreted polypeptides they encode
PT   - useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders
PS   Claim 1; Page 190-191; 447pp; English.
CC   This sequence represents a nucleic acid molecule which encodes a secreted
CC   human protein.  The gene number, and the clone it is derived from, are
CC   detailed in the descriptor line.  The gene can be used to generate fusion
CC   proteins by linking to the gene to a human immunoglobulin Fc portion
CC   (e.g. V34145) for increasing the stability of the fused protein as
CC   compared to the human protein only.
CC   The invention relates to 70 novel genes and their fragments (nucleic acid
CC   sequences: V34154-V34276; amino acid sequences W75057-W75179) which
CC   are useful for preventing, treating or ameliorating  medical conditions
CC   e.g. by protein or gene therapy.  Also, pathological conditions can be
CC   diagnosed by determining the amount of the new polypeptides in a sample
CC   or by determining the presence of mutations in the new polynucleotides.
CC   Specific uses are described for each of the 70 polynucleotides, based on
CC   which tissues they are most highly expressed in (see V34154 for described
CC   uses).
SQ   Sequence   2378 BP;    518 A;    690 C;    662 G;    506 T;


alignment_scores:
            Quality:  221.00              Length:    242
              Ratio:  1.601                Gaps:     11
 Percent Similarity:  57.025   Percent Identity: 30.992

alignment_block:
 US-08-962-560A-4 x V34188   ..

 Align seg 1/1  to: V34188  from: 1  to: 2378

      20 ArgArgArgSerGluProSerSerSerSerSerSerSerSerProAlaAl 36
         |||||||||:::|||               |||:::   :::|||:::||
      17 CGCCGCCGCGCAGAA.............TCCACGCTGGCTCCGTGCGC 51

      36 aProValArgProArgProCysProAlaValProAlaProAlaProGlyA 53
         |   |||               ||||||:::             |||  |
      52 CATGGTCACCCACAGCAAGTTTCCCGCCGCCGGGATGAGCCGCCCCCTGG 101

      53 spThrHisPheArg......ThrPheArgSerHisSerAspTyrArgArg 67
         |||||  :::|||     ||||||  |||  |||:::|||:::
     102 ACACCAGCCTGCGCCTCAAGACCTTCAGCTCCAAGAGCGAGTACCAGCTG 151

      68 IleThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTyrTrpGlyPr 84
         :::::::::  ||||||  ::::::     ||||||||||||:::
     152 GTGGTGAACGC.AGTGCGCAAGTGCAGGAGAGCGGCTTCTACTGGAGCGC 200

      84 oLeuSerValHisGlyAlaHisGluArgLeuArgAlaGluProValGlyT 101
         ::::::        |||:::     |||  ||||||||||:::||||
     201 AGTGACCGGCGGCGAGGCGAACCTGCTGCTCAGTGCCGAGCCCGCCGGCA 250

     101 hrPheLeuValArgAspSer.ArgGlnArgAsnCysPhePheAlaLeuSe 117
         ||||||||:::|||||||||| |||:::::::::   ||||||:::||||
     251 CCTTTCTGATCCGCGACAGCTCGGGACCAGCGCCACTTCTTCACGCTCAG 300

     117 rValLysMetAlaSerGlyProThrSerIleArgValHisPheGlnAlaG 134
         |||||||      ||||||      ::::::|||::::::   :::::::|
     301 CGTCAAGACCCAGTCTGGGACCAAGAACCTGCGCATCCAGTGTGAGGGGG 350

     134 lyArgPheHisLeuAspGlySer...ArgGluThr..............  144
         ||   |||   |||:::::::::   |||:::|||
     351 GCAGCTTCTCTCTGCAGAGCGATCCCCGGAGCACGCAGCCCGTGSCCCGC 400

     145 PheAspCysLeuPheGluLeuLeuGluHisTyrVal.............  156
         |||||||||:::::::::|||:::::::||||||:::
     401 TTCGACTGCGTGCTCAAGCTGGTGCACCACTACATGCCGCCCCCTGGAGC 450

     156 ..............................................  156

     451 CCCCTCCTTCCCCTCGCCACCTACTGAACCCTCCTCCGAGGTGCCCGAGC 500

     157 .........................AlaAlaProArgArg.........  161
                                 :::   |||||||||
     501 AGCCGTCTGCCCAGCCACTCCCTGGGAGTCCCCCCAGAAGAGCCTATTAC 550

     162 ............................MetLeuGlyAlaProLeuAr 168
                                     :::|||:::   ||||||
     551 ATCTACTCCGGGGGCGAGAAGATCCCCCTGGTGTTGAGCCGGCCCCTC.. 598

     168 gGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleValA 185
          :::   :::|||      ||||||:::|||||||||:::   :::   :
     599 .TCCTCCAACGTGGCCACTCTTCAGCATCTCTGTCGGAAGACCGTCAACG 647

     185 laAlaVal...GlyArgGluAsnLeuAlaArgIleProLeuAsnProVal 200
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     648 GCCACCTGGACTCCTATGAGAAAGTCACCCAGCTGCCG...GGGCCCATT 694

     201 LeuArgAspTyrLeuSerSerPhe 208
         |||:::::::|||:::::::::
     695 ...CGGGAGTTCCTGGACCAGTAC 715

seq_name: N_Geneseq_36:V38681

seq_documentation_block:
ID   V38681 standard; DNA; 848 BP.
AC   V38681;
DT   27-OCT-1998  (first entry)
DE   Homo sapiens SOCS11 gene.
KW   SOCS; suppressor of cytokine signalling; PCR primer;
KW   autoimmune disease; diagnosis; cancer; treatment;
KW   cytokine mediated cellular responsiveness; hyperimmunity;
KW   immunosuppression; allergies; hypertension; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1. .624
FT                   /*tag= a
FT                   /product= SOCS11 protein
PN   WO9820023-A1.
PD   14-MAY-1998.
PF   31-OCT-1997; AU0729.
PR   14-FEB-1997; AU-005117.
PR   01-NOV-1996; AU-003384.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Alexander WS, Hilton DJ, Metcalf D, Nicholson SE,
PI   Nicola NA, Richardson RT, Starr R, Viney EM, Willson TA;
DR   WPI; 98-286854/25.
DR   P-PSDB; W62623.
PT   Suppressor of cytokine signalling proteins - useful to treat
PT   disease, injury or abnormality involving cytokine mediated cellular
PT   responsiveness e.g. hyperimmunity, immunosuppression, allergies and
PT   hypertension
PS   Claim 14; Page 157-158; 325pp; English.
CC   The sequence is that of a gene encoding a suppressor of cytokine
CC   signalling protein (SOCS). SOCS can be used to screen for naturally
CC   occurring antibodies to SOCS, which may occur, e.g. in some autoimmune
CC   diseases. Alternatively, specific antibodies can be used to
CC   screen for SOCS, which is useful as a knowledge of SOCS levels
CC   may be important for the diagnosis of certain cancers. Soluble
CC   SOCS polypeptides can be used to treat disease, injury or
CC   abnormality involving cytokine mediated cellular responsiveness,
CC   e.g. hyperimmunity, immunosuppression, allergies and hypertension.
SQ   Sequence   848 BP;    224 A;    215 C;    207 G;    202 T;


alignment_scores:
            Quality:  147.50              Length:    157
              Ratio:  1.799                Gaps:      2
 Percent Similarity:  52.229   Percent Identity: 26.752

alignment_block:
 US-08-962-560A-4 x V38681   ..
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Align seg 1/1  to: V38681  from: 1  to: 848

     75 LeuAspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAlaHi 91
        |||:::   ||||||:::|||||||||||||:::::   :::   |||::
      1 TTGGAGAAGTGTGGTTGGTATTGGGGGCCAATGAATTGGGAAGATGCAGA 50

     91 sGluArgLeuArgAlaGluProValGlyThrPheLeuValArgAspSerA 108
        :   :::|||::::::::::|||   |||:::|||||||||||||||||||
     51 GATGAAGCTGAAAGGGAAACCAGATGGTTCTTTCCTGGTACGAGACAGTT 100

    108 rgGlnArgAsnCysPhePheAlaLeuSerValLysMetAlaSerGlyPro 124
          :::   :::   ::::::::::||||||   :::      :::
    101 CTGATCCTCGTTACATCCTGAGCCTCAGTTTCCGATCACAGGGTATCACC 150

    125 ThrSerIleArgValHisPheGlnAlaGlyArgPheHisLeu..... 138
                |||:::::::         |||   |||   |||
    151 CACCACACTAGAATGGAGCACTACAGAGGAACCTTCAGCCTGTGGTGTCA 200

    139 .............AspGlySerArgGluThrPheAspCysLeuPheGluL 151
                    |||      :::::::::   :::   :::   :::
    201 TCCCAAGTTTGAGGACCGCTGTCAATCTGTTGTAGAGTTTATTAAGAGAG 250

    151 euLeuGluHis..................................... 154
          :::   |||
    251 CCATTATGCACTCCAAGAATGGAAAGTTTCTCTATTTCTTAAGATCCAGG 300

    155 .........TyrValAlaAlaProArgArgMetLeuGlyAlaProLeuAr 168
                     :::|||  :::::::|||              ||
    301 GTTCCAGGACTGCCACCAACTCCTGTCCAGCTGCTCTATCCAGTGTCCCG 350

    168 gGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleValA 185
        |      :::|||:::   ||||||:::|||||||||   ||||||
    351 ATTCAGCAATGTCAAATCCCTCCAGCACCTTTGCAGATTCCGGATACGAC 400

    185 laAlaValGlyArgGluAsnLeuAlaArgIleProLeuAsnProValLeu 201
            |||      :::::::::      :::||||||         |||
    401 AGCTCGTCAGGATAGATCACATCCCAGATCTCCCACTGCCTAAACCTCTG 450

    202 ArgAspTyrLeuSerSerPhe 208
        :::|||:::   :::|||
    451 ATCTCTTATATCCGAAAGTTC 471

seq_name: N_Geneseq_36:V38668

seq_documentation_block:
ID   V38668 standard; DNA; 1221 BP.
AC   V38668;
DT   27-OCT-1998  (first entry)
DE   Homo sapiens SOCS5 gene.
KW   SOCS; suppressor of cytokine signalling; PCR primer;
KW   autoimmune disease; diagnosis; cancer; treatment;
KW   cytokine mediated cellular responsiveness; hyperimmunity;
KW   immunosuppression; allergies; hypertension; ss.
OS   Homo sapiens.
PN   WO9820023-A1.
PD   14-MAY-1998.
PF   31-OCT-1997; AU0729.
PR   14-FEB-1997; AU-005117.
PR   01-NOV-1996; AU-003384.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Alexander WS, Hilton DJ, Metcalf D, Nicholson SE,
PI   Nicola NA, Richardson RT, Starr R, Viney EM, Willson TA;
DR   WPI; 98-286854/25.
PT   Suppressor of cytokine signalling proteins - useful to treat
PT   disease, injury or abnormality involving cytokine mediated cellular
PT   responsiveness e.g. hyperimmunity, immunosuppression, allergies and
PT   hypertension
PS   Disclosure; Page 134-135; 325pp; English.
CC   The sequence is that of a gene encoding a suppressor of cytokine
CC   signalling protein (SOCS). SOCS can be used to screen for naturally
CC   occurring antibodies to SOCS, which may occur, e.g. in some autoimmune
CC   diseases. Alternatively, specific antibodies can be used to
CC   screen for SOCS, which is useful as a knowledge of SOCS levels
CC   may be important for the diagnosis of certain cancers. Soluble
CC   SOCS polypeptides can be used to treat disease, injury or
CC   abnormality involving cytokine mediated cellular responsiveness,
CC   e.g..hyperimmunity, immunosuppression, allergies and hypertension.
SQ   Sequence   1221 BP;    347 A;    259 C;    275 G;    340 T;


alignment_scores:
            Quality:  145.00            Length:    142
              Ratio:  1.790               Gaps:      4
 Percent Similarity:  57.042   Percent Identity: 29.577

alignment_block:
 US-08-962-560A-4 x V38668   ..

 Align seg 1/1  to: V38668  from: 1  to: 1221

     81 TyrTrpGlyProLeuSerValHisGlyAlaHisGluArgLeuArgAlaGl 97
        |||||||||   ::::::   :::   |||:::      |||:::::::::
    446 TACTGGGGAGTGATGGACCGTTATGAAGCAGAAGCCCTTCTCGAAGGGAA 495

     97 uProValGlyThrPheLeuValArgAspSerArgGlnArgAsnCysPheP 114
        :|||   |||||||||||||:::|||||||||   |||::::::   ||||
    496 ACCTGAAGGCACGTTTTTGCTCAGGGACTCTGCGCAAGAGGACTACTTCT 545

    114 heAlaLeuSerValLysMetAlaSerGlyProThrSerIleArgValHis 130
        ||:::::::|||   :::      :::               |||::::::
    546 TCTCTGTGAGCTTCCGCCGATACAACAGATCCCTGCATGCCCGAATTGAG 595

    131 PheGlnAlaGlyArgPheHisLeuAspGlySerArgGluThrPheAspCy 147
                  :::|||   :::|||:::                ||
    596 CAGTGGAATCACAACTTTAGTTTCGACGCCCATGAC.........CCGTG 636

    147 sLeuPheGlu.................LeuLeuGluHisTyrValAlaA 158
        |:::|||:::                |||||||||||||||
    637 TGTATTTCACTCCTCCACTGTAACGGGACTTTTAGAACATTATAAAGATC 686

    158 laProArgArgMetLeuGlyAlaProLeu.........ArgGlnArgArg 171
                  |||:::      ||||||               :::|||
    687 CCAGTTCGTGCATGTTTTTTGAACCATTGCTTACTATATCACTAAATAGG 736

    172 ValArgPro......LeuGlnGluLeuCysArgGlnArgIleValAlaAl 186
        :::   |||      ||||||   :::||||||      |||      ::
    737 ACTTTCCCTTTTAGCCTGCAGTATATCTGTCGCGCGGTAATCTGCAGGTG 786

    186 aValGlyArgGluAsnLeuAlaArgIleProLeuAsnProValLeuArgA 203
        ::::      :::::::::      :::||||||      :::|||:::|
    787 CACTACGTATGATGGAATTGATGGGCTCCCTCTACCCTCAATGTTACAGG 836

    203 spTyrLeuSerSerPheProPheGln 211
        ||:::|||:::::::::  ::::::
    837 ATTTTTTAAAAGAGTATCATTATAAA 862

seq_name: N_Geneseq_36:V38687

seq_documentation_block:
ID   V38687 standard; cDNA; 2438 BP.
AC   V38687;
DT   27-OCT-1998  (first entry)
DE   Mus musculus SOCS14 cDNA.
KW   SOCS; suppressor of cytokine signalling; PCR primer;
KW   autoimmune disease; diagnosis; cancer; treatment;
KW   cytokine mediated cellular responsiveness; hyperimmunity;
KW   immunosuppression; allergies; hypertension; ss.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   CDS             2. .1630
FT                   /*tag= a
FT                   /product= SOCS14 protein
PN   WO9820023-A1.
PD   14-MAY-1998.
PF   31-OCT-1997; AU0729.
```

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PR   14-FEB-1997; AU-005117.
PR   01-NOV-1996; AU-003384.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Alexander WS, Hilton DJ, Metcalf D, Nicholson SE,
PI   Nicola NA, Richardson RT, Starr R, Viney EM, Willson TA;
DR   WPI; 98-286854/25.
DR   P-PSDB; W62625.
PT   Suppressor of cytokine signalling proteins - useful to treat
PT   disease, injury or abnormality involving cytokine mediated cellular
PT   responsiveness e.g. hyperimmunity, immunosuppression, allergies and
PT   hypertension
PS   Claim 14; Page 165-167; 325pp; English.
CC   The sequence is that of a gene encoding a suppressor of cytokine
CC   signalling protein (SOCS). SOCS can be used to screen for naturally
CC   occurring antibodies to SOCS, which may occur, e.g. in some autoimmune
CC   diseases. Alternatively, specific antibodies can be used to
CC   screen for SOCS, which is useful as a knowledge of SOCS levels
CC   may be important for the diagnosis of certain cancers. Soluble
CC   SOCS polypeptides can be used to treat disease, injury or
CC   abnormality involving cytokine mediated cellular responsiveness,
CC   e.g. hyperimmunity, immunosuppression, allergies and hypertension.
SQ   Sequence   2438 BP;    676 A;    483 C;    556 G;    721 T;


alignment_scores:
           Quality:  138.50            Length:    217
             Ratio:  1.248               Gaps:      9
 Percent Similarity:  51.152   Percent Identity: 26.267

alignment_block:
 US-08-962-560A-4 x V38687   ..

 Align seg 1/1  to: V38687  from: 1  to: 2438

       8 AlaAlaAspAsnAlaIleSerProAlaAlaGluProArgArgArgSerGl 24
         |||   :::::::::|||||||||:::::::::   :::||||||||||
    1029 GCTCCAGAAAAAGGAATAAGCCCAGGTGGGAAATGGAAGAGGAGATCCTG 1078

      24 uProSerSerSerSerSerSerSerProAlaAlaProVal.ArgPro 40
                        ||||||:::|||   :::   ::: ||||||
    1079 CAGTTGGAGGCACCTCCTAAGTTCCACACCCAGATCG...ACTACGTCCA 1125

      41 ArgProCysProAlaValProAlaProAlaProGlyAspThrHisPheAr 57
            ||||||   :::   |||
    1126 CTGCCTTGTTCCANACCTCCT..........................  1146

      57 gThrPheArgSerHisSerAspTyr.ArgArgIleThrArgThrSerAla 73
                       ||||||    :::
    1147 ................TCAGATCAGTAAC.....................  1159

      74 LeuLeuAspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAl 90
            :::   |||      |||||||||   ::::::   :::::::||
    1160 ......AATCCGTGC......TACTGGGGTGTCATGGACAAATATGCAGC 1197

      90 aHisGluArgLeuArgAlaGluProValGlyThrPheLeuValArgAspS 107
         |:::      |||::::::::::|||   ||||||||||||:::|||||||
    1198 CGAAGCTCTGCTGGAAGGAAAGCCAGAGGGCACCTTTTTACTTCGAGATT 1247

     107 erArgGlnArgAsnCysPhePheAlaLeuSerValLysMetAlaSerGly 123
         ||   |||::::::   :::|||::::::|||   :::      |||
    1248 CAGCGCAGGAAGATTATTTATTCTCTGTTAGTTTTAGACGCTACAGTCGT 1297

     124 ProThrSerIleArgValHisPheGlnAlaGlyArgPheHisLeuAspGl 140
                    |||::::::             :::|||   :::|||::
    1298 TCTCTTCATGCTAGAATTGAGCAGTGGAATCATAACTTTAGCTTTGATGC 1347

     140 ySerArgGluThrPheAspCysLeuPheGlu.................L 151
         :                  |||:::|||:::                 |
    1348 CCATGAT.........CCTTGTGTCTTCCATTCTCCTGATATTACTGGGC 1388

     151 euLeuGluHisTyrValAlaAlaProArgArgMet.............. 162
         ||||||||||||||                 |||
    1389 TCCTGGAACACTATAAGGACCCCAGTGCCTGTATGTTCTTTGAGCCGCTC 1438

      163 LeuGlyAlaProLeuArgGlnArgArgValArgProLeuGlnGluLeuCy 179
          |||:::::::||||||   :::                |||||:::::||
     1439 TTGTCCACTCCCTTAATCCGGACGTTCCCCTTTTCCTTGCAGCATATTTG 1488

      179 sArgGlnArgIleValAlaAlaValGlyArgGluAsnLeuAlaArgIleP 196
          ||||      |||      ::::::      :::::::::      :::|
     1489 CAGAACGGTTATTTGTAATTGTACGACTTACGATGGCATCGATGCCCTTC 1538

      196 roLeuAsnProValLeuArgAspTyrLeuSerSerPheProPheGln 211
          ||:::         ::::::   ||||||:::::::::   ::::::
     1539 CCATTCCTTCGCCTATGAAATTGTATCTGAAGGAATACCATTATAAA 1585

seq_name: N_Geneseq_36:V71075

seq_documentation_block:
ID   V71075 standard; cDNA; 2532 BP.
AC   V71075;
DT   08-FEB-1999  (first entry)
DE   Green fluorescent protein-protein tyrosine phosphatase 1C fusion product.
KW   Human; protein tyrosine phosphatase 1C gene; fusion protein;
KW   green fluorescent protein; GFP; intracellular signalling; chimera; ss.
OS   Chimeric - Aequorea victoria.
OS   Chimeric - Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1. .2532
FT                   /*tag= a
PN   WO9845704-A2.
PD   15-OCT-1998.
PF   07-APR-1998; DK0145.
PR   07-APR-1997; DK-000392.
PA   (NOVO ) NOVO-NORDISK AS.
PI   Kasper A, Petersen Bjorn S, Scudder K, Thastrup O,
PI   Tullin S;
DR   WPI; 98-594491/50.
DR   P-PSDB; W85030.
PT   Determining effect on signalling pathways in live cells from
PT   redistribution of luminophores - specifically fusions of green
PT   fluorescent protein with a signalling component, and new apparatus,
PT   particularly for identifying toxins and potential therapeutic agents
PS   Claim 63; Pages 213-217; 326pp; English.
CC   The present sequence encodes a green fluorescent protein (GFP)-human
CC   protein tyrosine phosphatase 1C fusion protein. The fusion protein is
CC   used in an assay to exemplify the invention. The specification describes
CC   how quantitative information about the influence of a molecule on a
CC   cellular response is obtained by recording the variation, caused by
CC   the molecule, on mechanically intact living cells, in the spatially
CC   distributed light emitted from a luminophore present in the cells. The
CC   variation in light emission is processed to provide information that
CC   correlates spatial distribution to the degree of the molecule. The method
CC   is used to identify agents that (in)directly affect intracellular
CC   signalling, especially to screen for potential therapeutic agents or
CC   toxins, and to identify new drug targets.
SQ   Sequence   2532 BP;    613 A;    742 C;    758 G;    419 T;


alignment_scores:
           Quality:  126.50            Length:    147
             Ratio:  1.421               Gaps:      7
 Percent Similarity:  60.544   Percent Identity: 34.694

alignment_block:
 US-08-962-560A-4 x V71075   ..

 Align seg 1/1  to: V71075  from: 1  to: 2532

      15 ProAlaAlaGluProArgArgArgSerGluProSerSerSerSerSerSe 31
         ||||||   :::|||:::|||||||   :::|||   :::::::::   ::
     549 CCAGCAGAACACCCCCATCGGCGA...CGGCCCCGTGCTGCTGCCCGACA 595

      31 rSerSerProAlaAlaProValArgProArgProCysProAlaValProA 48
         :      |||      ||||||||||||:::      |||          |
     596 ACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAG 645
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 48 laProAlaProGlyAspThrHisPheArg...ThrPheArgSerHisSer 63
    ||   :::   |||   :::      |||         |||:::||||||
646 CGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCT 695

 64 AspTyrArgArgIle......ThrArgThrSerAlaLeuLeuAspAla.C 78
       :::   |||         :::||||||:::         ||||||
696 CGGCATGGACGAGCTGTACAAGTCCGGACTCAGATCTCGAGAGATGCTGT 745

 78 ys...GlyPheTyrTrpGlyProLeuSerValHisGlyAlaHisGluArg 93
       |||::::::         ||||||         |||:::
746 CCCGTGGGTGGTTTCACCGAGACCTCAGTGGGCTGGATGCAGAGACCCTG 795

 94 LeuArgAlaGluProVal...GlyThrPheLeuValArgAspSerArgGl 109
    |||::::::::::   |||   |||:::||||||:::|||   ||||||::
796 CTCAAGGGCCGAGGTGTCCACGGTAGCTTCCTGGCTCGGCCCAGTCGCAA 845

109 nArgAsnCysPhePheAlaLeuSerValLysMetAlaSerGlyProThrS 126
    :::::::      |||:::||||||||:::::::::::      |||
846 GAACCAGGGTGACTTCTCGCTCTCCGTCAGGGTGGGGGATCAGGTGACCC 895

126 erIleArgValHisPheGlnAlaGlyArgPheHisLeuAspGlySerArg 142
      ||||||::::::   ::::::      :::   |||   |||:::
896 ATATTCGGATCCAGAACTCAGGGGATTTCTATGACCTGTATGGAGGG... 942

143 GluThrPheAspCysLeuPheGluLeuLeuGluHisTyr 155
    |||   |||      |||   ||||||:::|||:::|||
943 GAGAAGTTTGCGACTCTGACAGAGCTGGTGGAGTACTAC 981
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